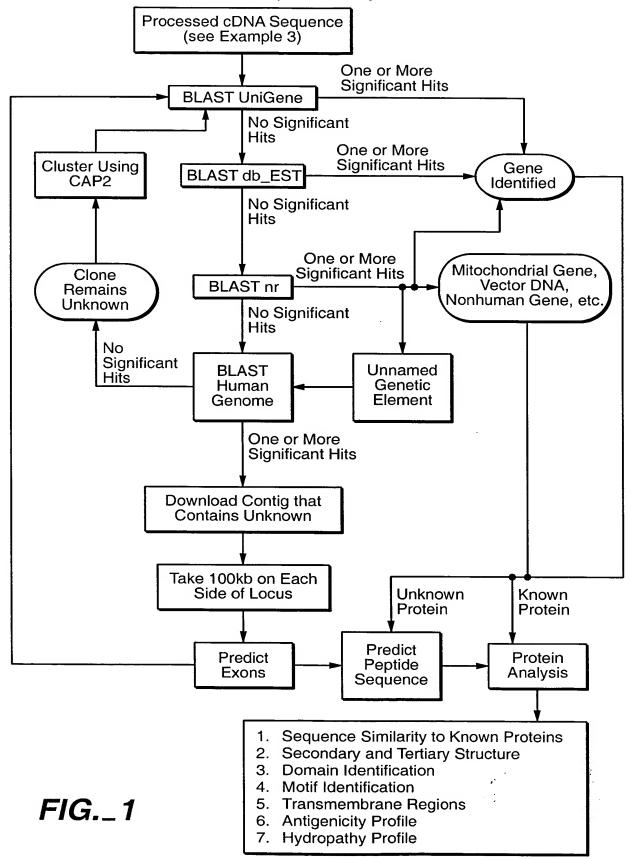
Leukocyte Expression Profiling tor: Jay WOHLGEMUTH Application No.: 10/006,290 Docket No: 506612000100

Sheet 1 of 11

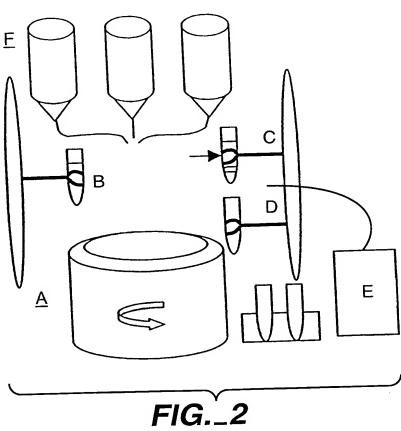
Novel Gene Sequence Analysis



Title: Leukocyte Expression Profiling Inventor: Jay WOHLGEMUTH Application No.: 10/006,290 Docket No: 506612000100

Sheet 2 of 11

Automated Mononuclear Cell RNA Isolation Device



Docket No: 506612000100

Sheet 3 of 11

Kits for Discovery of, or Application of Diagnostic Gene Sets

A. Contents of kit for discovery of diagnostic gene sets

- 1. Sterile, endotoxin and RNAse free blood collection tubes (>10cc capacity)
- 2. Alcohol swabs, tourniquet, 18g needle and syringe (>10cc capacity)
- 3. Erythrocyte lysis buffer
- 4. Leukocyte lysis buffer
- 5. Substrates for labeling of RNA (may vary for various expression profiling techniques)

For fluorescence cDNA microarray expression profiling:

Reverse transcriptase and 10x RT buffer

Poly-dT primer

DTT

Deoxynucleotides 100mM each

RNAse inhibitor

Cy3 and Cy5 labeled deoxynucleotides

- 6. cDNA microarrays containing candidate gene libraries
- 7. Cover slips for slides
- 8. hybridization chambers
- 9. Software package for identification of diagnostic gene set from data

Contains statistical methods.

Allows alteration in desired sensitivity and specificity of gene set.

Software facilitates access to and data analysis by centrally located database

- 10. Password and account number to access central database server.
- 11. Kit User Manual

B. Contents of kit for application of diagnostic gene sets

- 1. Sterile, endotoxin and RNAse free blood collection tubes (>10cc capacity)
- 2. Alcohol swabs, tourniquet, 18g needle and syringe (>10cc capacity)
- 3. Erythrocyte lysis buffer
- 4. Leukocyte lysis buffer
- 5. Substrates for labeling of RNA (may vary for various expression profiling techniques)

For fluorescence cDNA microarray expression profiling:

Reverse transcriptase and 10x RT buffer

Poly-dT primer

DTT

Deoxynucleotides 100mM each

RNAse inhibitor

Cy3 and Cy5 labeled deoxynucleotides

- 6. cDNA microarrays containing diagnostic gene sets
- 7. cover slips for slides
- 8. hybridization chambers
- 9. Software package for identification of diagnostic gene set from data

Contains statistical methods.

Allows alteration in desired sensitivity and specificity of gene set.

Software facilitates access to and data analysis by centrally located database

- 10. Password and account number to access central database server.
- 11. Kit User Manual

Title: Leukocyte Expression Profiling Inventor: Jay WOHLGEMUTH Application No.: 10/006,290 Docket No: 506612000100

Sheet 4 of 11

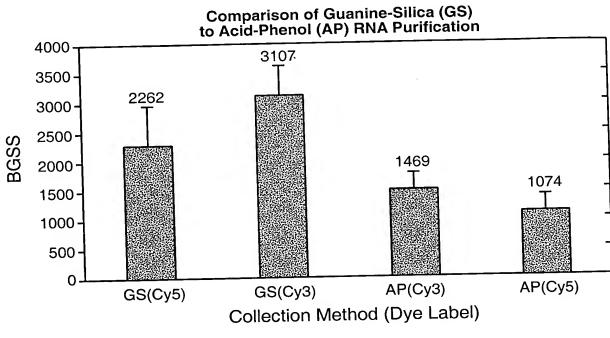


FIG._4

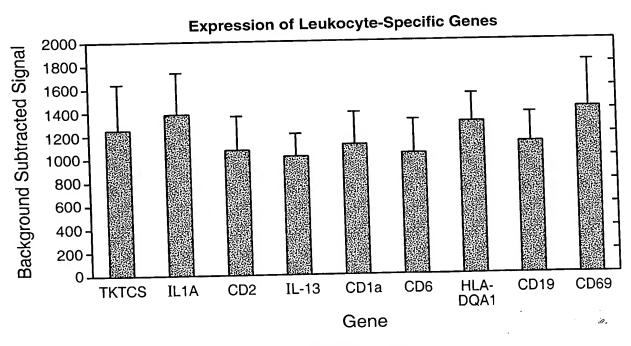


FIG._5

Title: Leukocyte Expression: Profiling: " """ Inventor: Jay WOHLGEMUTH Application No.: 10/006,290 Docket No: 506612000100

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Expression of Leukocyte-Specific Genes

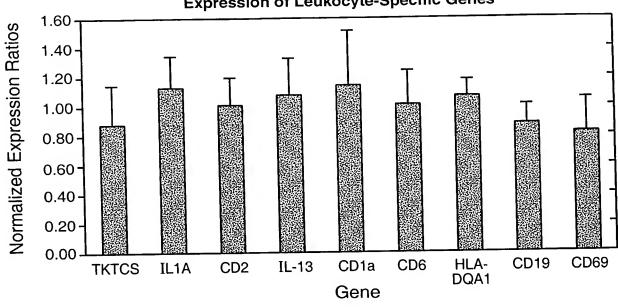


FIG._6

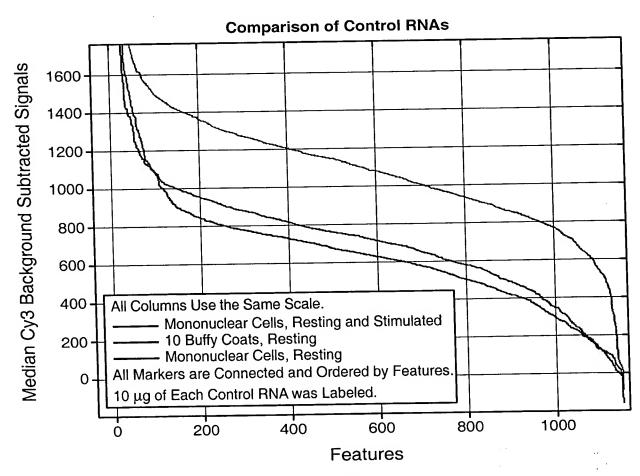


FIG._7

Title: Leukocyte Expression Profiting Inventor: Jay WOHLGEMUTH Application No.: 10/006,290 Docket No: 506612000100

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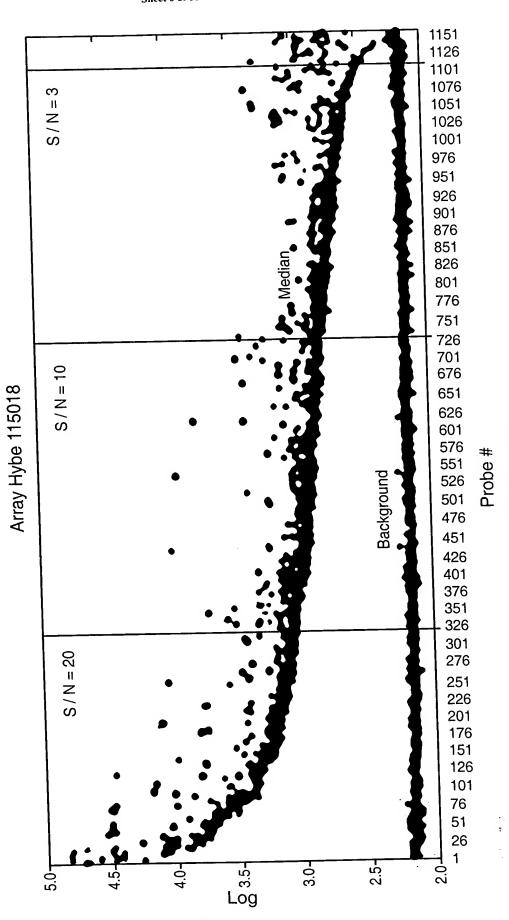
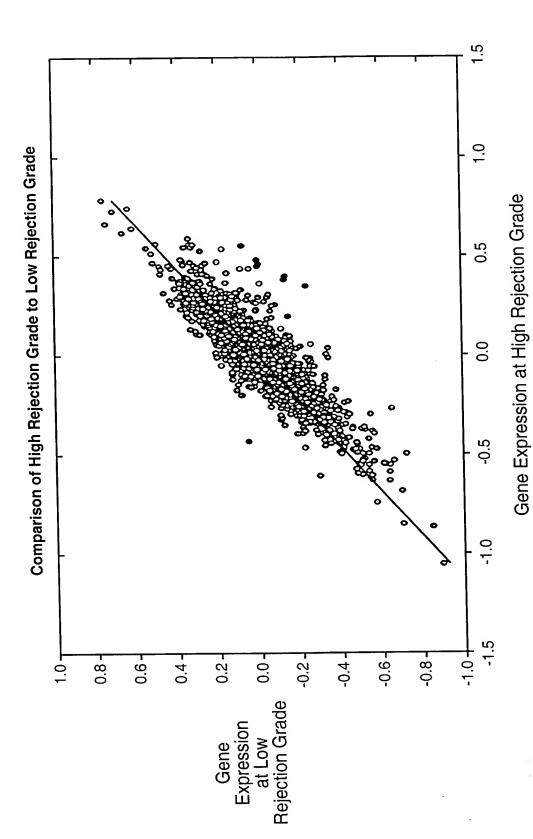


FIG. 8

Deukocyte Expression Profiling br: Jay WOHLGEMUTH Approaction No.: 10/006,290 Docket No: 506612000100 Sheet 7 of 11



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=1G._ 10A

Differential Gene Expression Between Grade 0 and 3A Samples:

Name F633 F100e Name Coligo ID B633 E532 Ratio G1/10 Itanscription factor 7 (T-cell specific, HMG-box) (TCF7), and principles of the companient of the compan	
Coligo ID Median -	
Oligo ID B633 B532 Ratio Ratio (9/1) 2476 5558 1050 0.188917 0.710038 HL 6025 1810 635 0.350829 1.318579 HL 6025 1804 95 0.18815 0.444098 S= 2407 804 95 0.118159 0.444098 TH 2283 13488 3477 0.25556 0.960516 TH 2283 13488 3477 0.25556 0.960516 TH 6025 1539 515 0.34623 1.25707 TH 6025 1539 515 0.34628 0.933154 TH 270 1119 0.24828 0.933154 TH 3729 1365 167 0.17894 0.672539 TH 3729 1365 167 0.17894 0.672539 TH 3729 1365 0.106047 0.398574 TH 3729 1365 0.106047 0.504771 TH 3720 1365 0.11218 0.421766 TH 3720 15538 2128 0.13895 0.514739 TH 3720 15538 0.111894 0.420551	
HL 6025 1810 635 0.188917 0.710038 HL 6025 1810 635 0.350829 1.318579 HL 6025 1402 487 0.347361 1.305545 S= 2407 804 95 0.118159 0.444098 S= 2407 805 1390 248 0.17894 0.672539 S= 2405 1390 248 0.178417 0.670576 S= 2405 1390 248 0.138591 0.520889 S= 2408 0.138591 0.520889 S= 2408 0.138591 0.520889 S= 2408 0.138591 0.420551 S= 24085 0.11894 0.11894 0.420551 S= 24085 0.11894 0.118851 0.11894 0.	OI
HL 6025 1810 635 0.350829 1.318579 HL 6025 1402 487 0.347361 1.305545 S= 2407 804 95 0.118159 0.444098 D6 2192 4121 405 0.098277 0.369371 Lt 2283 13488 3477 0.25556 0.960516 HL 6025 1539 515 0.334633 1.257707 HL 6025 3850 386 0.10026 0.376823 D1 13581 4507 1119 0.24828 0.933154 D2 476 2716 486 0.17894 0.459827 D1 2476 2716 486 0.17894 0.459827 D2 2192 3357 356 0.106047 0.398574 D3 2192 3357 356 0.106047 0.398574 D2 2192 235 0.11655 0.6072 D2 2192 3357 356 0.116341 0.670576 D3 3790 15538 2128 0.13695 0.514739 D2 3790 15538 2128 0.13695 0.514739 D3 3791 11974 1558 0.11894 0.420551	box) (TCF7),
HL 6025 1402 487 0.347361 1.305545 S= 2407 804 95 0.118159 0.444098 D6 2192 4121 405 0.098277 0.369371 HL 6025 1539 3477 0.2556 0.960516 HL 6025 1539 515 0.334633 1.257707 D6 2192 3850 386 0.10026 0.376823 D1 2476 2716 486 0.17894 0.672539 D2 2192 3357 356 0.106047 0.398574 D6 24905 1390 248 0.177847 0.670576 D6 24905 1390 248 0.177674 0.645231 D6 24905 1390 248 0.171674 0.645231 D7 3790 15538 2128 0.13695 0.514739 D7 3790 15538 2128 0.13015 0.489034 D7 3791 11974 1558 0.111894 0.420551	DQ beta 1 (HL
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2192 4121 405 0.098277 0.369371 2283 13488 3477 0.25556 0.960516 6025 1539 3477 0.25556 0.960516 1539 3477 0.25556 0.960516 2192 3850 386 0.10026 0.376823 3581 4507 1119 0.24828 0.933154 2476 2716 486 0.17894 0.672539 642 9850 5254 0.533401 2.004771 2192 3357 356 0.106047 0.398574 2192 3357 356 0.106047 0.398574 24905 1390 248 0.178417 0.670576 24905 1390 248 0.178417 0.670576 24905 1390 248 0.178417 0.670576 24905 1390 248 0.178417 0.670576 2595 0.116218 0.421766 2595 0.112218 0.421766 2595 0.112218 0.421766 2595 0.112218 0.481139 2590 11974 1558 0.138591 0.520889 2790 15538 2128 0.130115 0.489034 2790 15538 2128 0.130115 0.489034 2770 0.111894 0.420551	mRNA / cds=
2283 13488 3477 0.25556 0.960516 66025 1539 515 0.334633 1.257707 1.2192 3850 386 0.10026 0.376823 1.257707 1119 0.24828 0.933154 0.459827 1365 167 0.17894 0.672539 0.17894 0.672539 0.17894 0.672539 0.17894 0.672539 0.17894 0.672539 0.17894 0.672539 0.17894 0.672539 0.17894 0.672539 0.17894 0.672539 0.17894 0.672539 0.17894 0.672539 0.106047 0.398574 0.398574 0.645231 0.6072 0.178417 0.645231 0.6072 0.10672 0.1	antigen) (CD6
6025 1539 515 0.334633 1.257707 1192 2192 3850 0.10026 0.376823 3581 4507 1119 0.24828 0.933154 0.459827 1365 167 0.172344 0.459827 0.17894 0.672539 0.17894 0.672539 0.17894 0.672539 0.17894 0.672539 0.17894 0.672539 0.17894 0.672539 0.106047 0.398574 0.533401 2.004771 0.2192 3357 356 0.106047 0.398574 0.60725 0.161555 0.6072 0.6072 0.161555 0.161555 0.6072 0.161555 0.161555 0.514739 0.13892 2128 0.138951 0.520889 0.136953 1.1974 1.558 0.11894 0.420551 0.489034 0.420551	ber 3) (LTB), tr
2192 3850 386 0.10026 0.376823 54 4507 1119 0.24828 0.933154 64507 1119 0.24828 0.933154 665990/0119 2476 2716 486 0.17894 0.672539 665990/0119 2192 3357 356 0.106047 0.398574 0.672531 2192 3357 356 0.106047 0.398574 0.672531 2192 240 0.178417 0.670576 24481 1826 295 0.178417 0.670576 0.161555 0.6072 295 0.112218 0.421766 3790 15538 2128 0.136955 0.514739 3791 11974 1558 0.130115 0.489034 3791 11974 1558 0.111894 0.420551	DQ beta 1 (HL
1 3581 4507 1119 0.24828 0.933154 983154 A 3729 1365 167 0.122344 0.459827 9650 642 9850 5254 0.17894 0.672539 9650 6 2192 3357 356 0.106047 0.398574 6 2192 3357 356 0.106047 0.398574 6 2192 3357 356 0.106047 0.398574 65 4905 1390 248 0.178417 0.670576 65 4481 1826 295 0.161555 0.6072 65 4481 1826 295 0.161555 0.6072 65 4481 6512 747 0.114711 0.421766 6 3761 6512 747 0.1136955 0.520889 6 37790 15538 2128 0.130115 0.420551 6 3761 6953 778 0.111894 0	antigen) (CD6
A 3729 1365 167 0.122344 0.459827 8650 642 9850 5254 0.533401 2.004771 6 2192 3357 356 0.106047 0.398574 6 2192 3357 356 0.106047 0.398574 7 3357 356 0.106047 0.398574 85 4905 1390 248 0.178417 0.670576 65 4905 1398 240 0.171674 0.645231 65 4481 1826 295 0.161555 0.6072 65 4481 6512 747 0.114711 0.431139 6 3761 6728 755 0.112218 0.421766 7 3790 8572 1188 0.138591 0.520889 8 3791 11974 1558 0.130115 0.489034 9 3791 11974 1558 0.111894 0.420551	tein 1 (FÙBP1
486 0.17894 0.672539 Edg 642 9850 5254 0.533401 2.004771 6 2192 3357 356 0.106047 0.398574 65 4905 1390 248 0.178417 0.670576 65 4905 1398 240 0.171674 0.6072 65 4481 1826 295 0.161555 0.6072 6 3761 6512 747 0.114711 0.431139 6 3751 6728 755 0.112218 0.421766 7 3790 15538 2128 0.138591 0.520889 8 3791 11974 1558 0.130115 0.489034 1 6953 778 0.111894 0.420551	mber 2 (NR4A
642 9850 5254 0.533401 2.004771 6 2192 3357 356 0.106047 0.398574 65 4905 1390 248 0.178417 0.670576 65 4481 1826 295 0.161555 0.6072 65 4481 1826 295 0.161555 0.6072 6 3761 6512 747 0.114711 0.421766 7 3790 8572 1188 0.138591 0.520889 8 3790 1558 2128 0.136955 0.514739 9 3790 1558 0.138951 0.489034 10 3791 11974 1558 0.118194 0.420551	a-box) (TCF7),
2192 3357 356 0.106047 4905 1390 248 0.178417 4905 1398 240 0.171674 4481 1826 295 0.161555 3761 6512 747 0.114711 3761 6728 755 0.112218 3790 8572 1188 0.138951 3790 15538 2128 0.136955 3791 11974 1558 0.111894 3761 6953 778 0.111894	be 1b mRNA,
4905 1390 248 0.178417 4905 1398 240 0.171674 4481 1826 295 0.161555 3761 6512 747 0.114711 3761 6728 755 0.112218 3790 8572 1188 0.138591 3790 15538 2128 0.136955 3791 11974 1558 0.130115 3761 6953 778 0.111894	antigen) (CD6
4905 1390 248 0.178417 4905 1398 240 0.171674 4481 1826 295 0.161555 3761 6512 747 0.114711 3761 6728 755 0.112218 3790 8572 1188 0.138591 3790 15538 2128 0.136955 3791 11974 1558 0.11894 3761 6953 778 0.111894	
4905 1390 248 0.178417 4905 1398 240 0.171674 4481 1826 295 0.161555 3761 6512 747 0.114711 3761 6728 755 0.112218 3790 8572 1188 0.138591 3790 15538 2128 0.136955 3791 11974 1558 0.130115 3761 6953 778 0.111894	
4905 1390 248 0.178417 4905 1398 240 0.171674 4481 1826 295 0.161555 3761 6512 747 0.114711 3761 6728 755 0.112218 3790 8572 1188 0.138591 3790 15538 2128 0.136955 3791 11974 1558 0.130115 3761 6953 778 0.111894	
4905 1398 240 0.171674 4481 1826 295 0.161555 3761 6512 747 0.114711 3761 6728 755 0.112218 3790 8572 1188 0.138591 3790 15538 2128 0.136955 3791 11974 1558 0.130115 3761 6953 778 0.111894	chain / cds=(65
55 4481 1826 295 0.161555 c 3761 6512 747 0.114711 c 3761 6728 755 0.112218 3790 8572 1188 0.138591 3790 15538 2128 0.136955 3791 11974 1558 0.130115 c 3761 6953 778 0.111894	chain / cds=(65
c 3761 6512 747 0.114711 c 3761 6728 755 0.112218 3790 8572 1188 0.138591 3790 15538 2128 0.136955 c 3761 6953 778 0.111894	chain / cds=(65
c 3761 6728 755 0.112218 3790 8572 1188 0.138591 3790 15538 2128 0.136955 3791 11974 1558 0.130115 c 3761 6953 778 0.111894	nain mRNA / c
3790 8572 1188 0.138591 3790 15538 2128 0.136955 3791 11974 1558 0.130115 c 3761 6953 778 0.111894	ain mRNA / c
3790 15538 2128 0.136955 3791 11974 1558 0.130115 c 3761 6953 778 0.111894	ly similar to
c 3761 11974 1558 0.130115 c 3761 6953 778 0.111894	ly similar to
n mRNA/c 3761 6953 778 0.111894	hly similar to
	n mRNA/

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FIG._ 10B

f SRs	Grade 3A / 0	0.30955069	0.31800317	0.31910959	0.32068403	0.33311587	0.33989617	0.3471323	0.34746767	0.35289603	0.35389672	0.3566264	0.36278818	0.37028503			4.68929496	4.73359863	4.95040579	5.37301111	5.48481867	5.50803866	5.61339689	5.65696646	5.71604612
Ratio of SRs	Grade 0 / 3A	3.23048873	3.14462275	3.13371968	3.11833431	3.00195843	2.94207495	2.88074602	2.87796556	2.83369583	2.82568319	2.80405488	2.75642938	2.70062225			0.21325167	0.21125576	0.20200364	0.18611538	0.18232143	0.18155283	0.17814525	0.17677319	0.1749461
Ą	SR: Scaled Ratio (g / r)	0.219793	0.419312	0.416612	0.142415	0.123043	0.326476	0.436591	0.130934	0.329306	0.162731	0.239845	0.727307	0.147586			3.144527	3.054262	3.005889	2,316513	2.313311	2.869076	2.889436	2.766449	2.403886
Array 107739: Grade 3A	Cv3 / Cv5 Ratio	0.061438	0.117209	0.116455	0.039809	0.034394	0.091259	0.122039	0.0366	0.09205	0.045488	0.067043	0.203302	0.041254			0.878982	0.853751	0,840229	0.647529	0.646634	0.801986	0.807677	0 773299	0.671952
Array 1077	F532 Median - B532	358	252	247	75	254	2727	237	282	220	434	356	197	246	CONTRACTOR CONTRACTOR		5767	6112	2498	17730	18636	13892	14245	18761	18560
	F633 Median - B633	5827	2150	2121	1884	7385	29882	1942	7705	0330	9541	5310	696	5963	March Control of the		6561	7159	2973	27381	0880	17322	17637	2/06/	27621

X72475	cDNA: FLJ21321 fis, clone COL02335, highly similar to	3791	10805	1411	0.130588	0.49081	
X72475	cDNA: FLJ21321 fis. clone COL02335, highly similar to	3790	11246	1453	0.129201	0.4856	
A F067420	SNC73 protein (SNC73) mRNA, complete cds / cds=(39	4399	2654	243	0.09156	0.344125	
X72/75	CONA FI. 121321 fis. clone COL02335. highly similar to	3791	10909	1370	0.125584	0.472005	
A FOR 7420	SNC73 protein (SNC73) mRNA, complete cds / cds=(39)	4399	1959	181	0.092394	0.34726	
A FOR 7420	SNC73 protein (SNC73) mRNA, complete cds / cds=(39)	4399	2558	215	0.08405	0.315899	
BC00963	rearranged imminoglobulin mRNA for mu heavy chain e	4474	7538	684	0.09074	0.341044	
BC002303	rearranged imminoglobilin mRNA for mu heavy chain e	4474	8662	780	0.090048	0.338444	
BC002363	rearranged imminophilip mRNA for mu heavy chain e	4474	7183	809	0.084644	0.318133	
BC002963	rearranged imminopolohi lin mRNA for mu heavy chain e	4475	9868	851	0.094703	0.355938	
BC002363	rearranged imminodobillin mRNA for mu heavy chain e	4476	11118	1023	0.092013	0.345828	
BC002363	rearranged imminorability mRNA for mu heavy chain e	4475	7428	730	0.098277	0.36937	
BC002963	rearranged imminorability mRNA for mu heavy chain e	4476	10413	933	0.0896	0.336757	
BC002363	rearranged imminorability mRNA for mu heavy chain e	4475	5841	484	0.082863	0.311436	
A ED67420	SNC73 protein (SNC73) mRNA complete cds / cds=(39	4398	7960	645	0.08103	0.304549	
VE067420	SNC73 protein (SNC73) mRNA complete cds / cds=(39	4398	11959	992	0.08295	0.311765	
AF067420	SNC73 protein (SNC73) mRNA, complete cds / cds=(39	4398	6161	447	0.072553	0.272689	

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FIG._ 10C

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tor: Jay WOHLGEMUTH
lication No.: 10/006,290
Docket No: 506612000100
Sheet 11 of 11

5.95900079	5.9816215	5.98789603	6.4924922	6.59109804	6.86979225	7.01342553	7.24745312	7.96186351	8.0748531	8.09993947	8.21727973	8.2606647	9.11364747	9.55378803	10.2010527	11.4716196	
0.16781337	0.16717875	0.16700357	0.15402406	0.15171979	0.14556481	0.14258368	0.13797951	0.12559874	0.12384126	0.12345771	0.12169477	0.12105563	0.10972555	0.10467052	0.0980291	0.08717165	
2.924735	2.904673	2.060585	3.064488	2.288826	2.170163	2.391889	2.45286	2.532931	2.874145	2.801184	3.035218	2.781837	2.838319	2.909599	3.180333	3.128181	
0.817544	0.811936	0.57599	0.856609	0.63979	0.60662	0.668599	0.685642	0.708024	0.803403	0.783008	0.848427	0.7776	0.793388	0.813313	0.888991	0.874413	
14334	13863	21610	18561	19369	21936	4037	2975	3909	1275	682	890	486	1344	18694	12597	14148	
17533	17074	37518	21668	30274	36161	6038	4339	5521	1587	871	1049	625	1694	22985	14170	16180	

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FIG10B	FIG 10D
FIG10A	FIG10C

FIG._ 10